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SEQUENCE LISTING

(1) GENERAL INFORMATION:

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Charette, Marc F
Cohen, Charles M
Crea, Roberto
Keck, Peter C
Oppermann, Hermann
Rueger, David C
Ridge, Richard J

(ii) TITLE OF INVENTION: Product and Process for the Production, Isolation and Purification of Recombinant Polypeptides

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Creative BioMolecules
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(C) CITY: Hopkinton
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 01748

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 07/661,070
(B) FILING DATE: 26-FEB-1991
(C) CLASSIFICATION: 435/68
536/27
530/300
530/350

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Lunn, Paul G.
(B) REGISTRATION NUMBER: 32,743
(C) REFERENCE/DOCKET NUMBER: CRP-008DV

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (508) 435-9001
(B) TELEFAX: (508) 435-6951

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ile Glu Gly Arg
1

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
GCT AAA AAC CTT AAC GAA GCT                                          21
Ala Lys Asn Leu Asn Glu Ala
  1               5
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ala Lys Asn Leu Asn Glu Ala
1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Lys Ala Ile Phe Val Leu Lys Gly Ser Leu Asp Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Lys Ala Ile Phe Val Leu Lys Gly Ser Leu Asp Arg Asp Leu Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Lys Ala Ile Phe Val Leu Lys Gly Ser Leu Asp Arg Asp Leu Asp
1 5 10 15

Ser Arg Leu Asp Leu Asp Val Arg Thr Asp His Lys Asp Leu Ser Asp
20 25 30

His Leu Val Leu Val Asp Leu Ala Arg Asn Asp Leu Ala Arg Ile Val
35 40 45

Thr Pro Gly Ser Arg Tyr Val Ala Asp Leu Glu
50 55

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Glu Phe Met Arg
1

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Glu Phe Asp Pro Pro Pro Lys Phe Met Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Glu Phe Asp Pro Pro Pro Met Pro Arg Lys Phe Met Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Glu Phe Asp Pro Pro Pro Met Pro Arg Met Pro Asp Pro Glu Leu Arg
1 5 10 15

Lys Phe Met Arg
20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Lys Ala Ile Phe Val Leu Lys Gly Ser Leu Asp Arg Asp Leu Asp
1 5 10 15

Ser Arg Ile Glu Leu Glu Met Arg Thr Asp His Lys Glu Leu Ser Glu
20 25 30

His Leu Met Leu Val Asp Leu Ala Arg Asn Asp Leu Ala Arg Ile Cys

```
319                35                  40                  45
320
321       Thr Pro Gly Ser Arg Tyr Val Ala Asp Leu Thr Lys Val Asp Arg Tyr
322           50                  55                  60
323
324       Ser Tyr Val Met His Leu Val Ser Arg Val Val Gly Glu Leu Arg His
325       65                  70                  75                  80
326
327       Asp Leu Asp Ala Leu His Ala Tyr Arg Ala Cys Met Asn Met Gly Thr
328                       85                  90                  95
329
330       Leu Ser Gly Ala Pro Lys Val Arg Ala Met Gln Leu Ile Ala Glu Ala
331                   100                 105                 110
332
333       Glu Gly Arg Arg Arg Gly Ser Tyr Gly Gly Ala Val Gly Tyr Phe Thr
334               115                 120                 125
335
336       Ala His Gly Asp Leu Asp Thr Cys Ile Val Ile Arg Ser Ala Leu Val
337           130                 135                 140
338
339       Glu Asn Gly Ile Ala Thr Val Gln Ala Gly Ala Gly Val Val Leu Asp
340       145                 150                 155                 160
341
342       Ser Val Pro Gln Ser Glu Ala Asp Glu Thr Arg Asn Lys Ala Arg Ala
343                       165                 170                 175
344
345       Val Leu Arg Ala Ile Ala Thr Ala His His Ala Gln Glu Phe Pro Gly
346                   180                 185                 190
347
348       Glu
349
350
351   (2) INFORMATION FOR SEQ ID NO:12:
352
353        (i) SEQUENCE CHARACTERISTICS:
354             (A) LENGTH: 59 amino acids
355             (B) TYPE: amino acid
356             (C) STRANDEDNESS: single
357             (D) TOPOLOGY: linear
358
359       (ii) MOLECULE TYPE: protein
360
361      (iii) HYPOTHETICAL: NO
362
363       (iv) ANTI-SENSE: NO
364
365        (v) FRAGMENT TYPE: N-terminal
366
367
368
369       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
370
371        Met Lys Ala Ile Phe Val Leu Lys Gly Ser Leu Asp Arg Asp Leu Asp
```

```
                1               5                   10                  15

Ser Arg Leu Asp Leu Asp Val Arg Thr Asp His Lys Asp Leu Ser Asp
            20                  25                  30

His Leu Val Leu Val Asp Leu Ala Arg Asn Asp Leu Ala Arg Ile Val
        35                  40                  45

Thr Pro Gly Ser Arg Tyr Val Ala Asp Leu Glu
    50                  55
```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
Met Lys Ala Ile Phe Val Leu Lys Gly Ser Leu Asp Arg Asp Leu Glu
1               5                   10                  15

Phe Met Pro Pro Cys
            20
```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

425
426
427 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
428
429 Met Lys Ala Ile Phe Val Leu Lys Gly Ser Leu Asp Arg Asp Leu Glu
430 1 5 10 15
431
432 Phe Met Cys
433

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/07/661,070

DATE: 04/22/91
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LINE	ERROR	ORIGINAL TEXT
35	Wrong application Serial Number	(A) APPLICATION NUMBER: US 07/661,070
36	Wrong Filing Date	(B) FILING DATE: 26-FEB-1991
37	Wrong Classification	(C) CLASSIFICATION: 435/68

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/07/661,070

DATE: 04/22/91
TIME: 09:27:54

MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA
APPLICATION NUMBER
FILING DATE

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/07/661,070

DATE: 04/22/91
TIME: 09:27:54

LINE ORIGINAL TEXT

CORRECTED TEXT